

FIG. 1

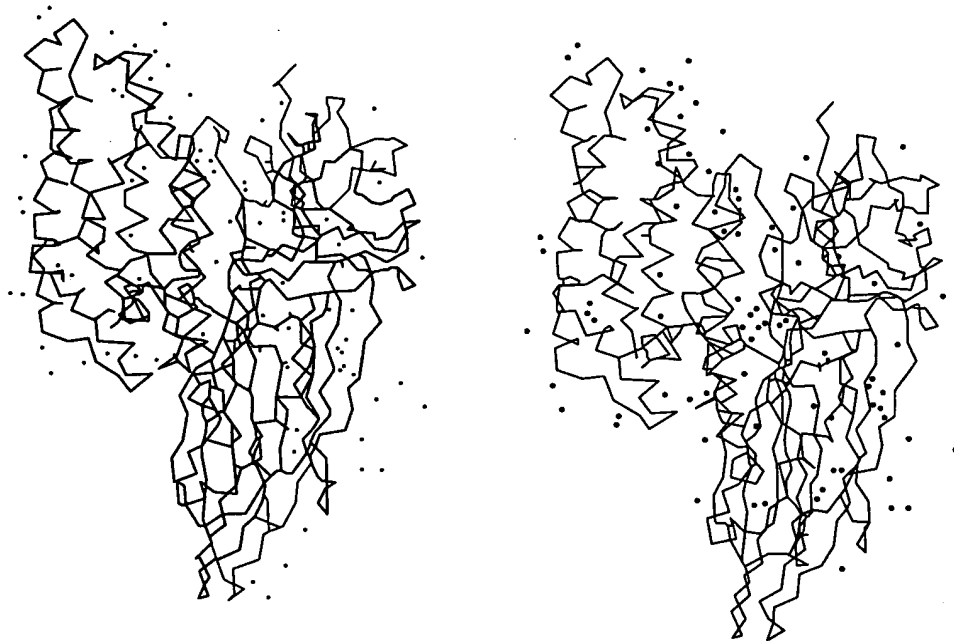


FIG. 2

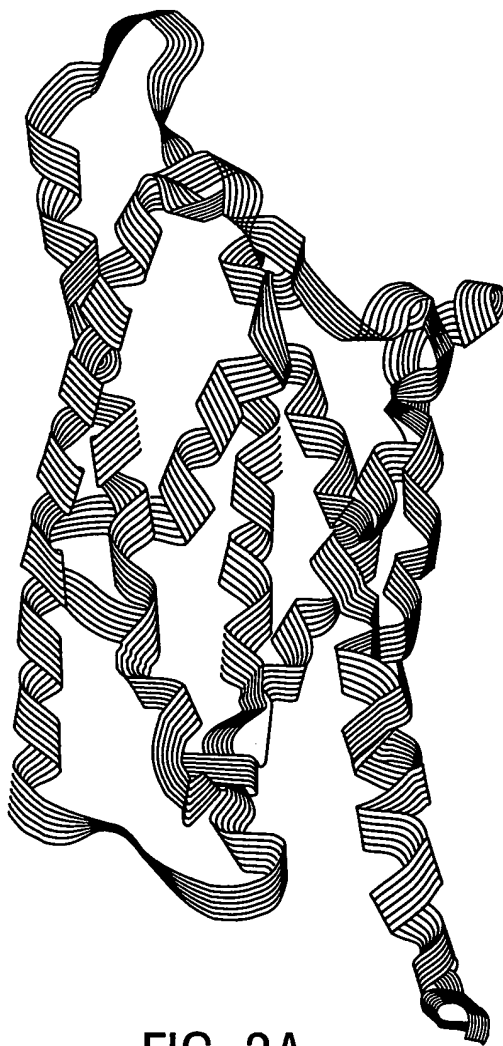


FIG. 3A

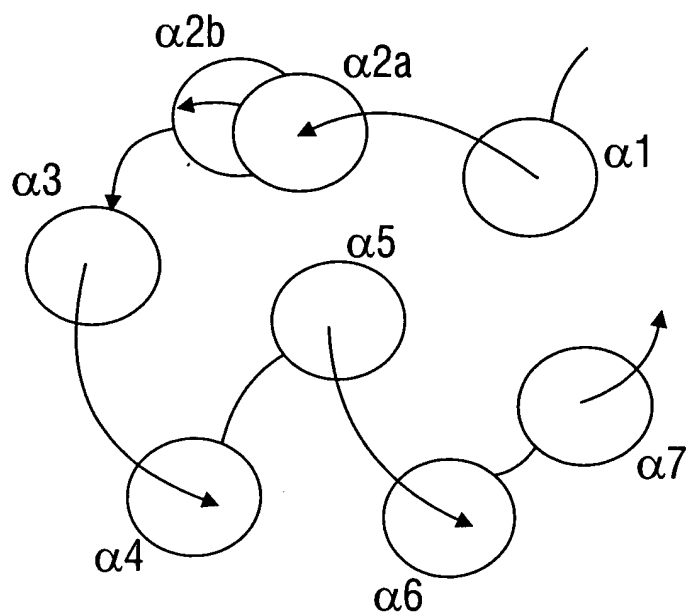


FIG. 3B

alpha helix	Amino acid Residues
$\alpha 1$	63-79
$\alpha 2a$	85-98
$\alpha 2b$	105-118
$\alpha 3$	124-153
$\alpha 4$	161-186
$\alpha 5$	194-215
$\alpha 6$	223-255
$\alpha 7$	260-286

FIG. 4

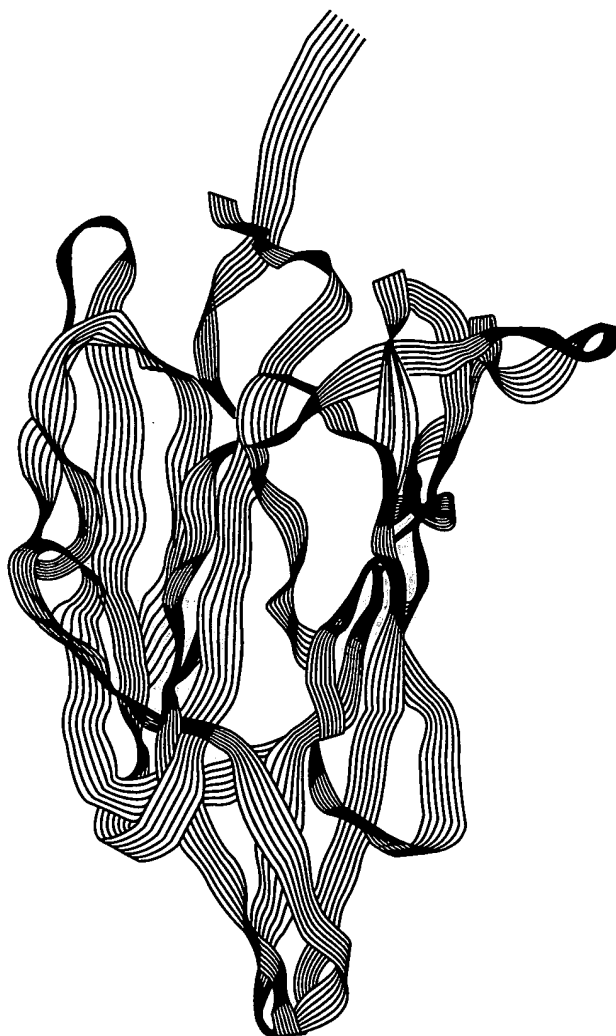


FIG. 5A

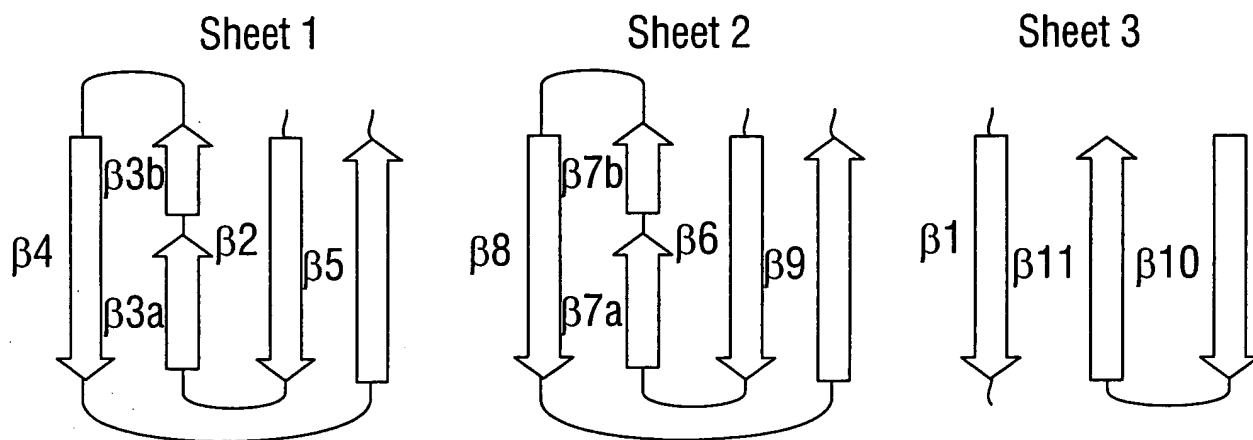


FIG. 5B

Sheet 1

β Strand	Amino Acid Residue
$\beta 2$	339-350
$\beta 3a$	256-360
$\beta 3b$	362-368
$\beta 4$	375-379
$\beta 5$	390-395

Sheet 2

β Strand	Amino Acid Residue
$\beta 6$	402-412
$\beta 7a$	416-419
$\beta 7b$	423-430
$\beta 8$	435-442
$\beta 9$	452-456

Sheet 3

β Strand	Amino Acid Residue
$\beta 1$	296-306
$\beta 10$	472-483
$\beta 11$	492-498

FIG. 6

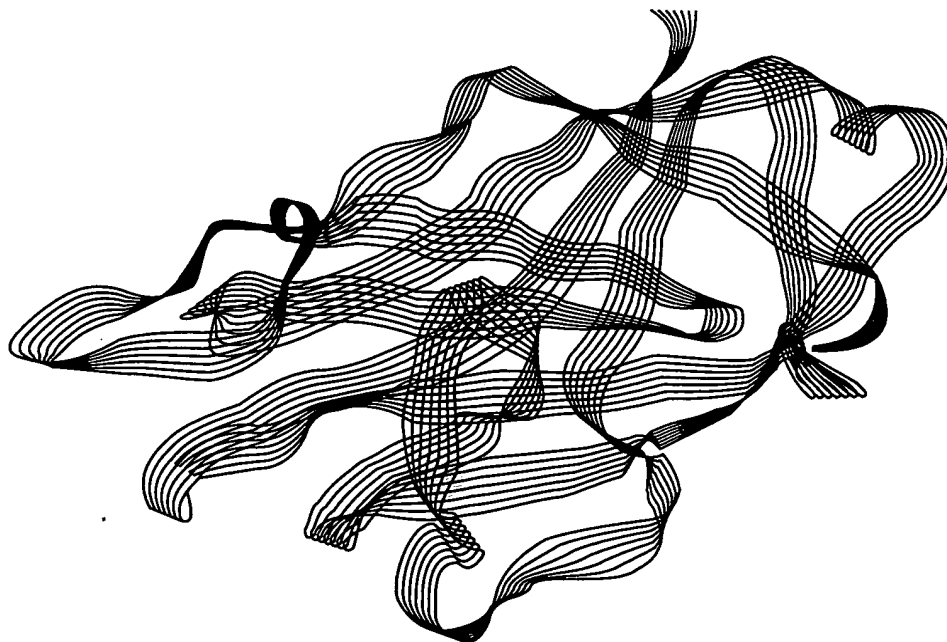


FIG. 7A

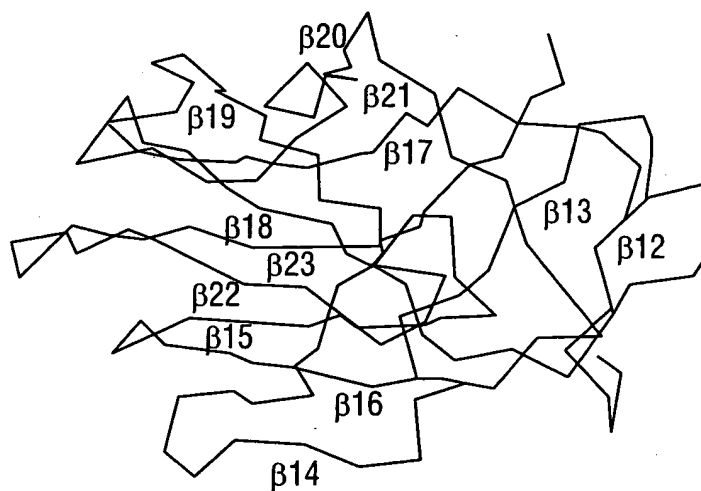


FIG. 7B

Strand Number	Amino Acid Residues
β 12	505-509
β 13	512-515
β 14	522-528
β 15	539-544
β 16	550-557
β 17	563-574
β 18	578-584
β 19	590-596
β 20	609-614
β 21	616-619
β 22	626-636
β 23	638-650

FIG. 8



FIG. 9A

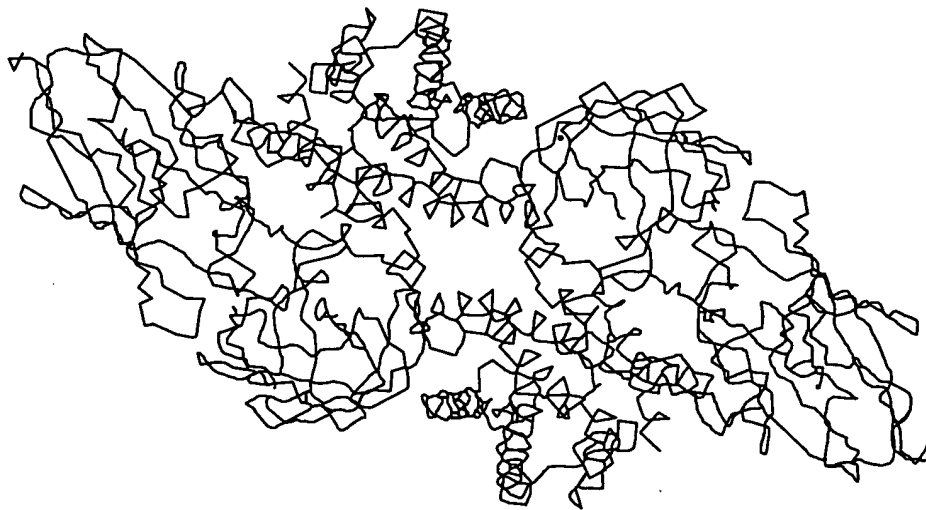


FIG. 9B

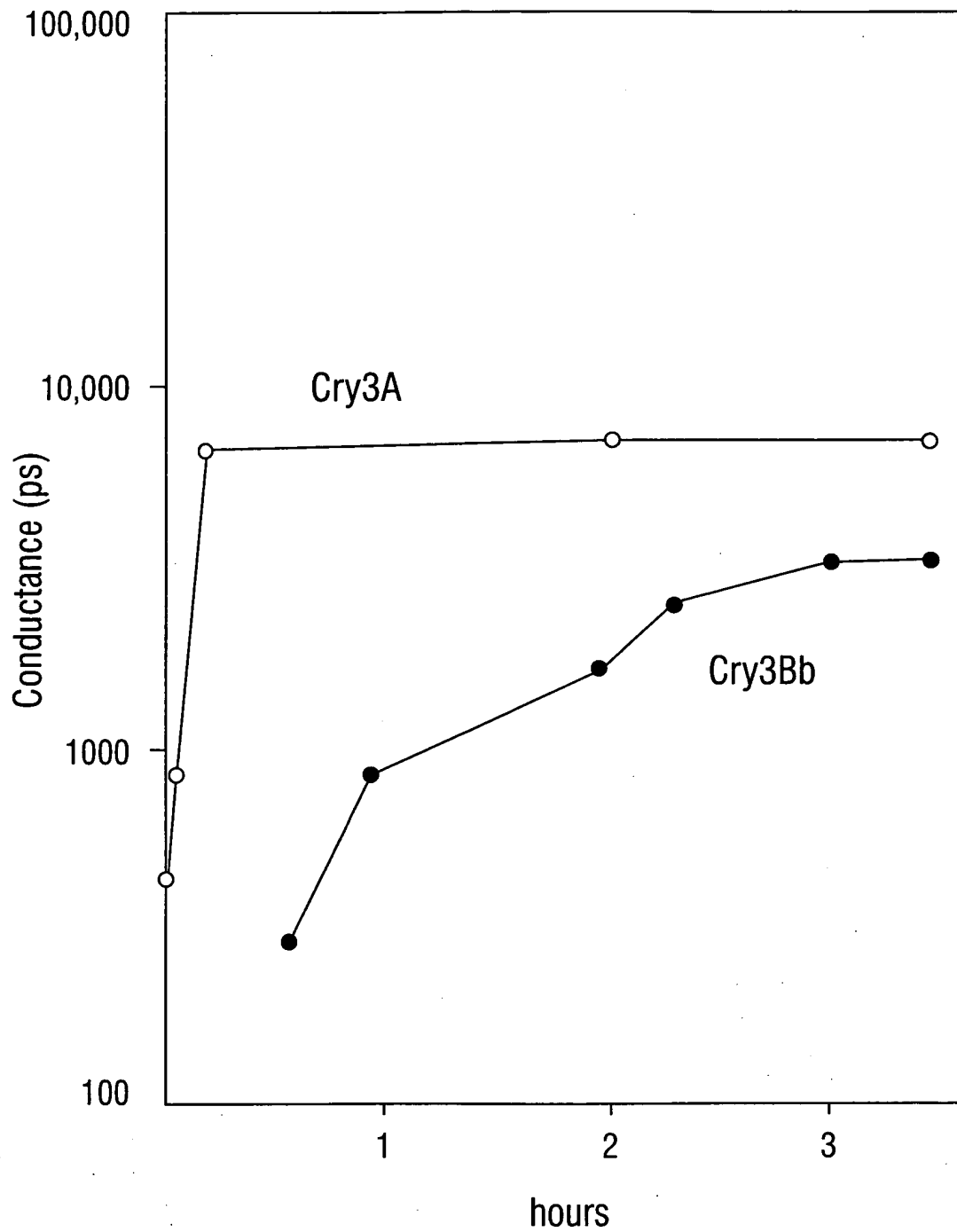


FIG. 10

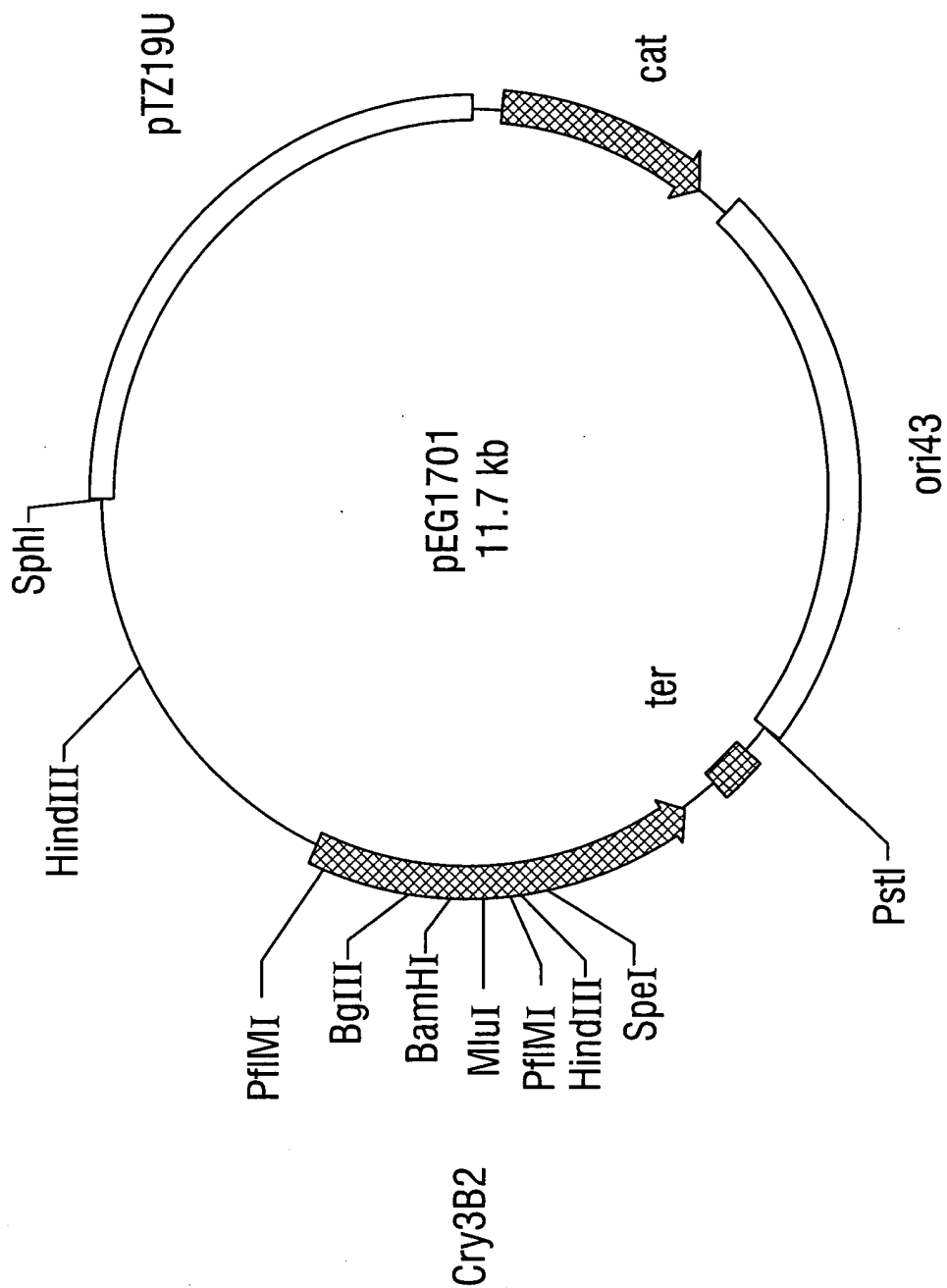


FIG. 11

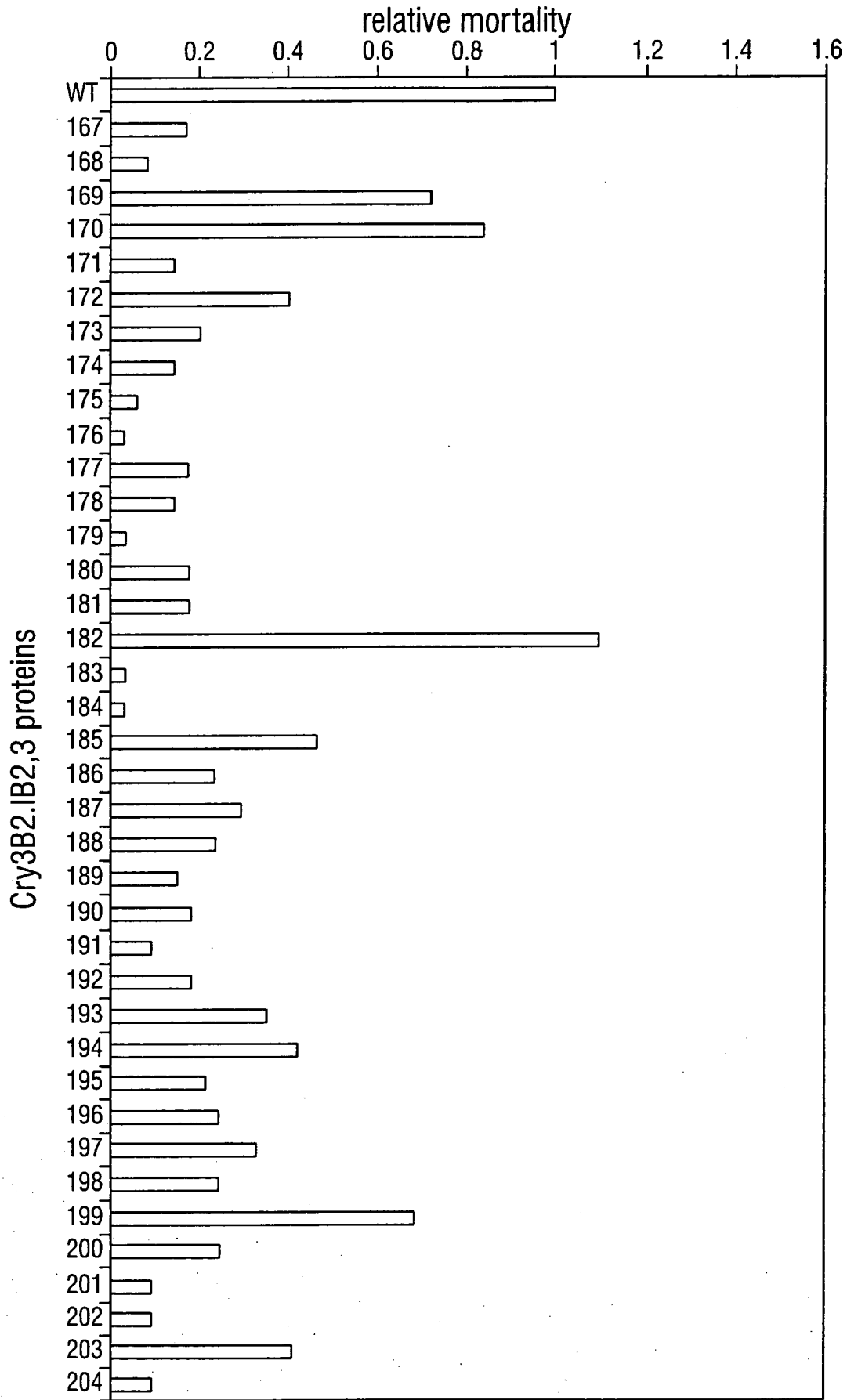


FIG. 12

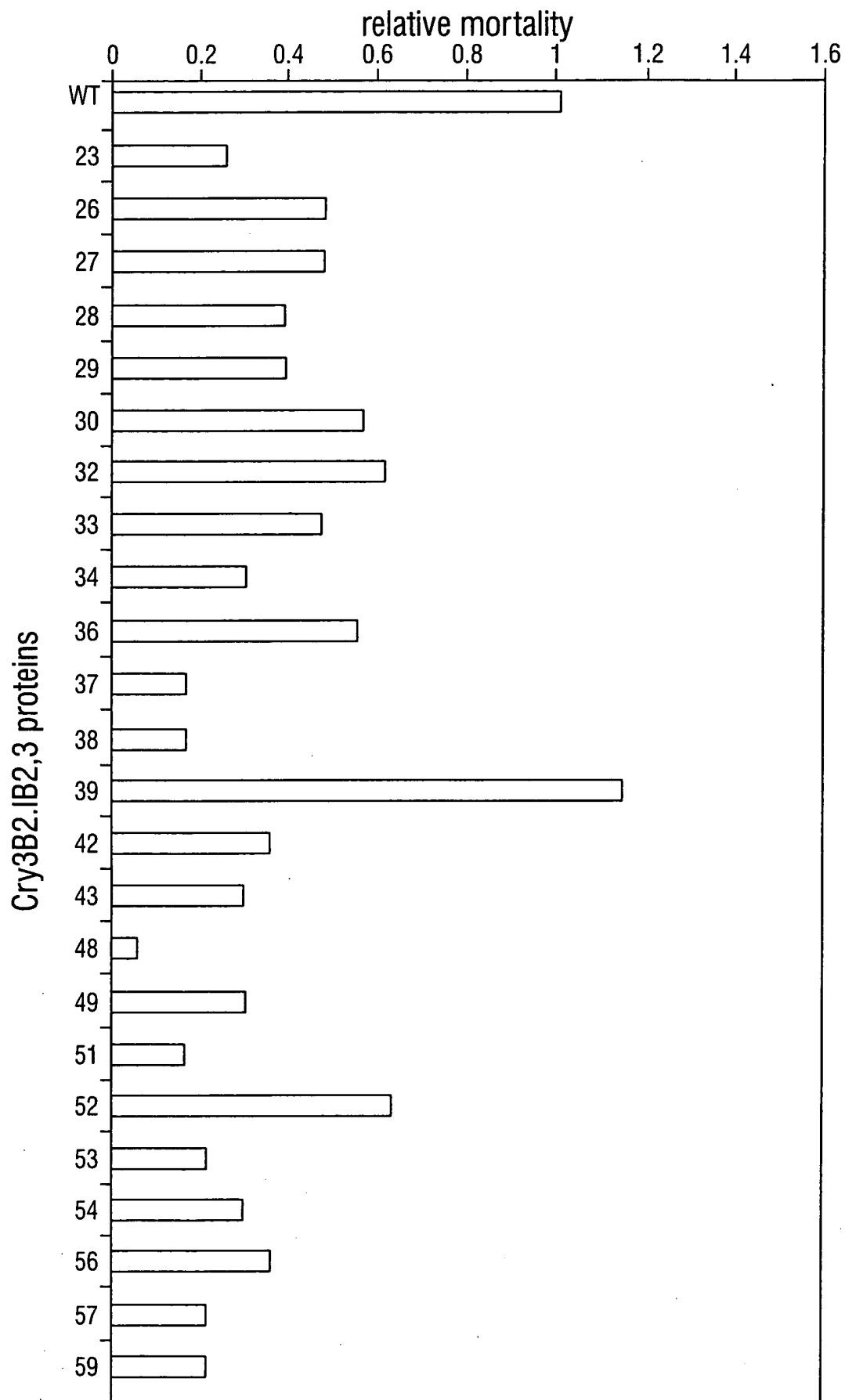


FIG. 13

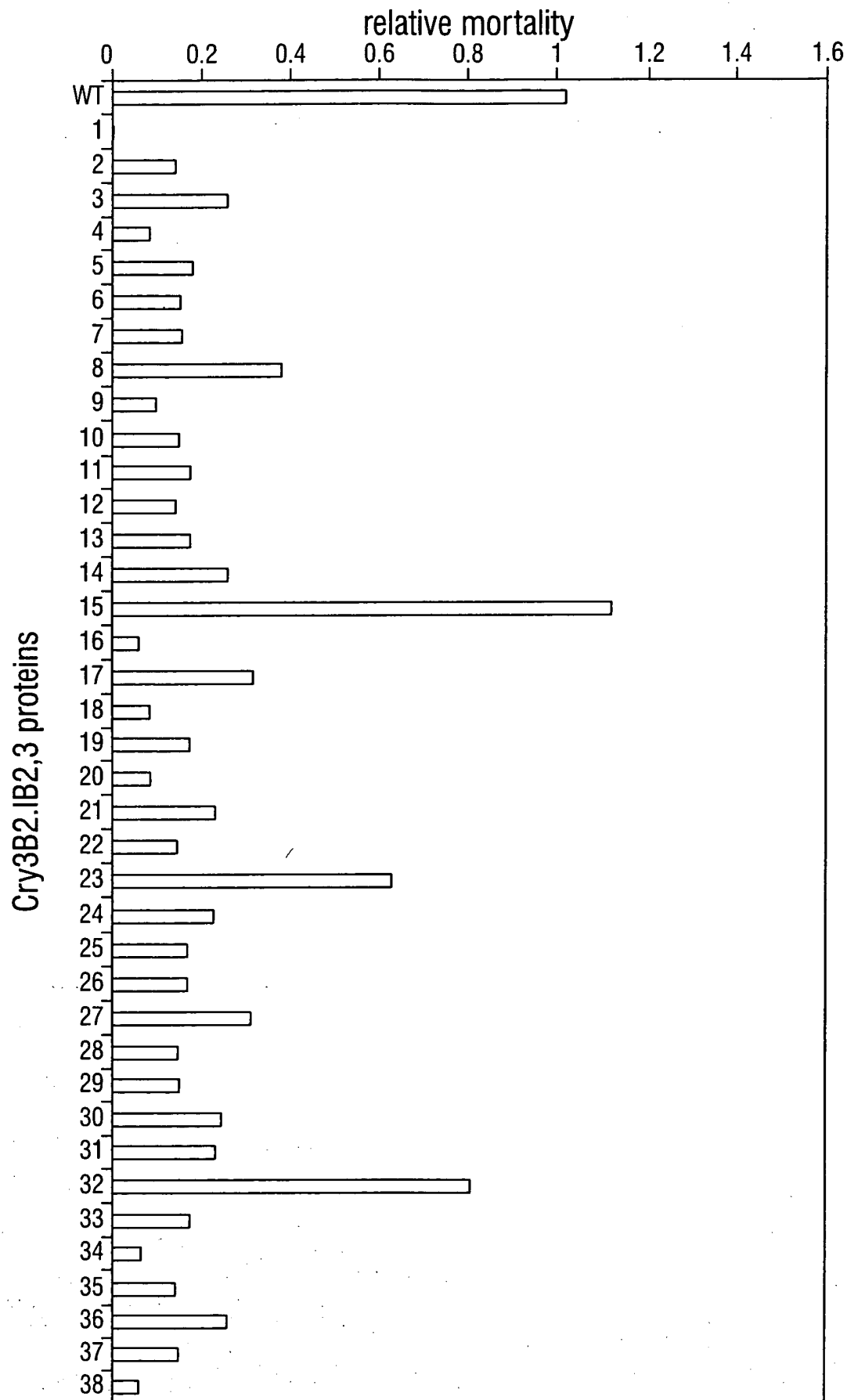


FIG. 14

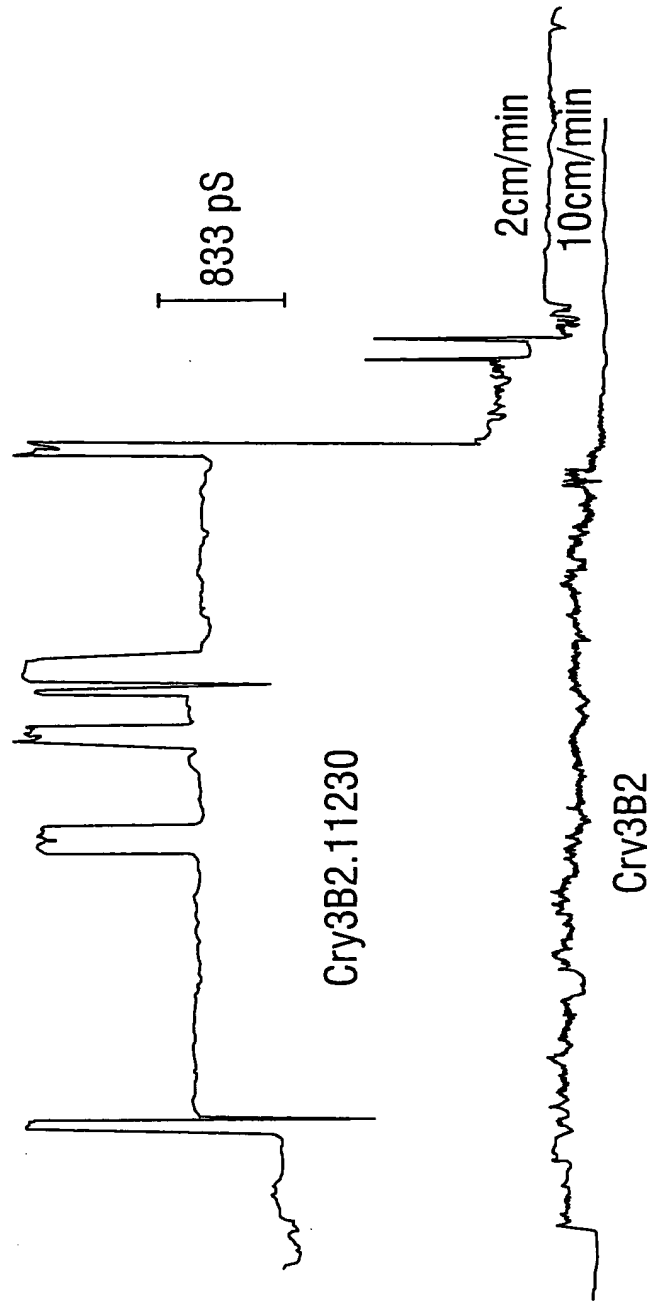


FIG. 15

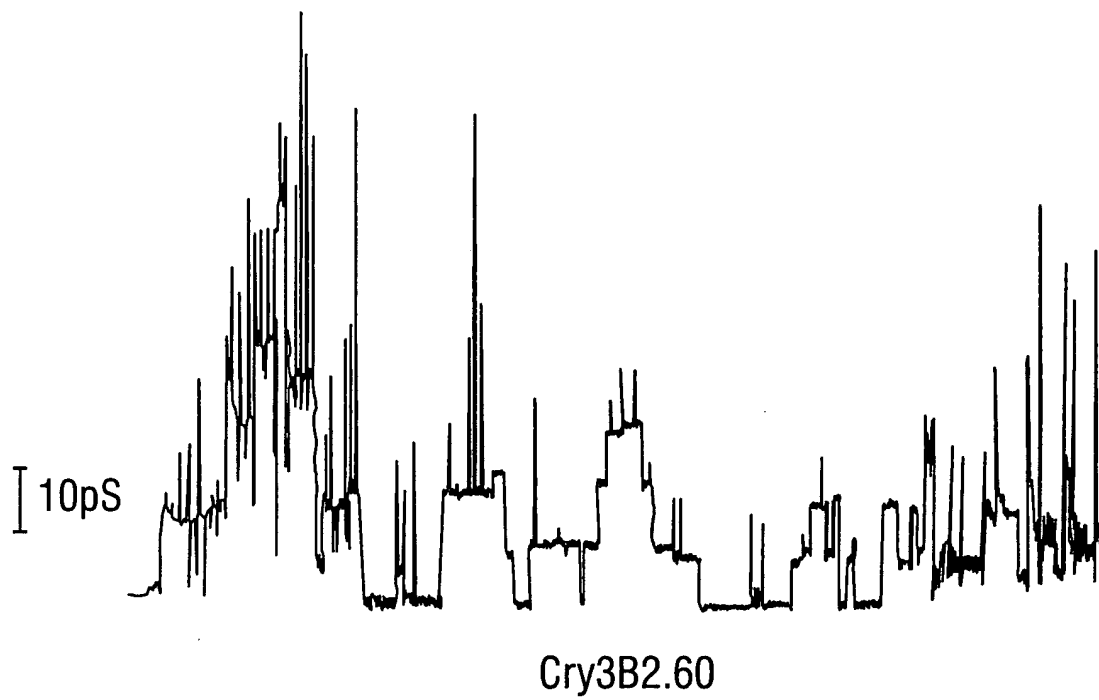
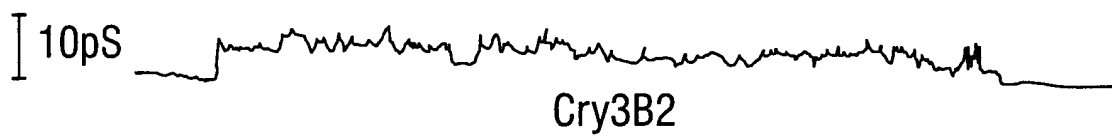


FIG. 16

ALIGNMENT OF CRY3 SEQUENCES

(Numbered according to Cry3BB)

(alpha helices underlined, beta sheets marked with + + +'s)

	1	10	20	30	40																																												
CRY3C:	M	N	P	N	R	S	E	H	D	I	K	A	T	E	N	N	E	V	S	N	N	H	A	Q	Y	P	L	A	D	T	P	-	-	T	L	E	E	L	N	Y									
CRYCBB2:	M	N	P	N	R	S	E	H	D	I	K	V	T	P	N	S	E	L	P	T	N	H	N	Q	Y	P	L	A	D	N	P	N	S	T	L	E	E	L	N	Y									
CRY3BB:	M	N	P	N	R	S	E	H	D	I	K	V	T	P	N	S	E	L	Q	T	N	H	N	Q	Y	P	L	A	D	N	P	N	S	T	L	E	E	L	N	Y									
CRY3BA:	M	I	R	M	G	G	R	K	M	N	P	N	R	S	E	Y	D	T	I	K	V	T	P	N	S	E	L	P	T	N	H	N	Q	Y	P	L	A	D	N	P	N	S	T	L	E	E	L	N	Y
CRY3A:	M	I	R	K	G	G	R	K	M	N	P	N	R	S	E	H	D	I	K	T	T	E	N	N	E	V	P	T	N	H	V	Q	Y	P	L	A	E	T	P	N	P	T	L	E	D	L	N	Y	

	50	60	70	80	90																																													
CRY3C:	K	E	F	L	R	R	T	D	N	N	V	E	A	L	D	S	T	T	K	D	A	I	Q	K	G	I	S	I	I	G	D	L	L	G	V	V	G	F	P	Y	G	G	A	L	V	S	F	Y		
CRYCBB2:	K	E	F	L	R	M	T	E	D	S	S	T	E	V	L	D	N	S	T	V	K	D	A	V	G	T	G	I	S	V	V	G	Q	I	L	G	V	V	G	V	P	F	A	G	A	L	T	S	F	Y
CRY3BB:	K	E	F	L	R	M	T	E	D	S	S	T	E	V	L	D	N	S	T	V	K	D	A	V	G	T	G	I	S	V	V	G	Q	I	L	G	V	V	G	V	P	F	A	G	A	L	T	S	F	Y
CRY3BA:	K	E	F	L	R	M	T	A	D	N	S	T	E	V	L	D	S	T	V	K	D	A	V	G	T	G	I	S	V	V	G	Q	I	L	G	V	V	G	V	P	F	A	G	A	L	T	S	F	Y	
CRY3A:	K	E	F	L	R	M	T	A	D	N	N	T	E	A	L	D	S	T	T	K	<u>D</u>	<u>V</u>	<u>I</u>	<u>Q</u>	<u>K</u>	<u>G</u>	<u>I</u>	<u>S</u>	<u>V</u>	<u>V</u>	<u>G</u>	<u>D</u>	<u>L</u>	<u>L</u>	<u>G</u>	<u>V</u>	<u>V</u>	<u>G</u>	<u>F</u>	<u>P</u>	<u>F</u>	<u>G</u>	<u>G</u>	<u>A</u>	<u>L</u>	<u>V</u>	<u>S</u>	<u>F</u>	<u>Y</u>	

	100	110	120	130	140																																													
CRY3C:	T	N	L	L	N	T	I	W	P	G	E	-	D	P	L	K	A	F	M	Q	Q	V	E	A	L	I	D	Q	K	I	A	D	Y	A	K	D	K	A	T	A	E	L	Q	G	L	K	N	V	F	K
CRY3BB2:	Q	S	F	L	D	T	I	W	P	S	D	A	D	P	W	K	A	F	M	A	Q	V	E	V	L	I	D	K	K	I	E	E	Y	A	K	S	K	A	L	A	E	L	Q	G	L	Q	N	N	F	E
CRY3BB:	Q	S	F	L	N	T	I	W	P	S	D	A	D	P	W	K	A	F	M	A	Q	V	E	V	L	I	D	K	K	I	E	E	Y	A	K	S	K	A	L	A	E	L	Q	G	L	Q	N	N	F	E
CRY3BA:	Q	S	F	L	N	A	I	W	P	S	D	A	D	P	W	K	A	F	M	A	Q	V	E	V	L	I	D	K	K	I	E	E	Y	A	K	S	K	A	L	A	E	L	Q	G	L	Q	N	N	F	E
CRY3A:	<u>T</u>	<u>N</u>	<u>F</u>	<u>L</u>	<u>N</u>	<u>T</u>	<u>I</u>	<u>W</u>	<u>P</u>	<u>S</u>	<u>E</u>	-	<u>D</u>	<u>P</u>	<u>W</u>	<u>K</u>	<u>A</u>	<u>F</u>	<u>M</u>	<u>E</u>	<u>Q</u>	<u>V</u>	<u>E</u>	<u>A</u>	<u>L</u>	<u>M</u>	<u>D</u>	<u>Q</u>	<u>K</u>	<u>I</u>	<u>A</u>	<u>D</u>	<u>Y</u>	<u>A</u>	<u>K</u>	<u>N</u>	<u>K</u>	<u>A</u>	<u>L</u>	<u>A</u>	<u>E</u>	<u>L</u>	<u>Q</u>	<u>G</u>	<u>L</u>	<u>Q</u>	<u>N</u>	<u>N</u>	<u>V</u>	<u>E</u>

	150	160	170	180	190																																													
CRY3C:	D	Y	V	S	A	L	D	S	W	D	K	T	P	L	T	L	R	D	G	R	S	Q	G	R	I	R	E	L	F	S	Q	A	E	S	H	F	R	R	S	M	P	S	F	A	V	S	G	Y	E	V
CRY3BB2:	D	Y	V	N	A	L	N	S	W	K	K	T	P	L	S	L	R	S	K	R	S	Q	D	R	I	R	E	L	F	S	Q	A	E	S	H	F	R	N	S	M	P	S	F	A	V	S	K	F	E	V
CRY3BB:	D	Y	V	N	A	L	N	S	W	K	K	T	P	L	S	L	R	S	K	R	S	Q	D	R	I	R	E	L	F	S	Q	A	E	S	H	F	R	N	S	M	P	S	F	A	V	S	K	F	E	V
CRY3BA:	D	Y	V	N	A	L	D	S	W	K	K	A	P	V	N	L	R	S	R	R	S	Q	D	R	I	R	E	L	F	S	Q	A	E	S	H	F	R	N	S	M	P	S	F	A	V	S	K	F	E	V
CRY3A:	<u>D</u>	<u>Y</u>	<u>V</u>	<u>S</u>	<u>A</u>	<u>L</u>	<u>S</u>	<u>S</u>	<u>W</u>	<u>Q</u>	<u>K</u>	<u>N</u>	<u>P</u>	<u>V</u>	<u>S</u>	<u>S</u>	<u>R</u>	<u>N</u>	<u>P</u>	<u>H</u>	<u>S</u>	<u>Q</u>	<u>G</u>	<u>R</u>	<u>I</u>	<u>R</u>	<u>E</u>	<u>L</u>	<u>F</u>	<u>S</u>	<u>Q</u>	<u>A</u>	<u>E</u>	<u>S</u>	<u>H</u>	<u>F</u>	<u>R</u>	<u>N</u>	<u>S</u>	<u>M</u>	<u>P</u>	<u>S</u>	<u>F</u>	<u>A</u>	<u>I</u>	<u>S</u>	<u>G</u>	<u>Y</u>	<u>E</u>	<u>V</u>

FIG. 17A

	200	210	220	230	240
CRY3C:	LFLPTYAQAANTHLLLLKDAQIYGTDWGYSTDDLNEFHTKQKDLTIEYTN				
CRY3BB2:	LFLPTYAQAANTHLLLLKDAQVFGEEWGYSSDVAEFYHRQLKLTQQYTD				
CRY3BB:	LFLPTYAQAANTHLLLLKDAQVFGEEWGYSSDVAEFYHRQLKLTQQYTD				
CRY3BA:	LFLPTYAQAANTHLLLLKDAQVFGEEWGYSSEDIAEFYQRQLKLTQQYTD				
CRY3A:	<u>LFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYTD</u>				

	250	260	270	280	290
CRY3C:	HCAKWYKAGLDKLRGSTYEEWVKFNRYRREMTLTVLDLITLFPYDVRTY				
CRY3BB2:	HCVNWYNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFYDVRLY				
CRY3BB:	HCVNWYNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFYDIRLY				
CRY3BA:	HCVNWYNVGLNSLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFYDVRLY				
CRY3A:	<u>HCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPYDVRLY</u>				

	300	310	320	330	340
CRY3C:	TKGVKTELTRDVLTDPIVAVNNMNGYGTTFSNIEYIRKPHLFDYLHAIQ				
CRY3BB2:	SKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLGIE				
CRY3BB:	SKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLGIE				
CRY3BA:	SKGVKTELTRDIFTDPIFTLNALQEYGPTFSSIENSIRKPHLFDYLRGIE				
CRY3A:	<u>PKEVKTELTRDVLTDPIVGNNLRGYGTTF</u> <u>SNIEYIRKPHLFDYLRHQ</u>				
	+++++				++++

	350	360	370	380	390
CRY3C:	FHSRLQPGYFGTDSFNYWSGNYVSTRSSIGSDEIIRSPFYGNKSTLDVQN				
CRY3BB2:	FHTRLQPGYSGKDSFNYWSGNYVETRPSIGSSKITSPFYGDKSTEPVQK				
CRY3BB:	FHTRLQPGYFGKDSFNYWSGNYVETRPSIGSSKITSPFYGDKSTEPVQK				
CRY3BA:	FHTRLRPGYSGKDSFNYWSGNYVETRPSIGSNDTITSPFYGDKSIEPIQK				
CRY3A:	<u>FHTRFQPGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEP</u> <u>VQN</u>				
	+++++	+++++	+++++	+++++	+++

	400	410	420	430
CRY3C:	LEFNGEKVFRAVANGNLAVWPVGTGGTKIHSGVTKVQFSQYNDRKDEVRT			
CRY3BB2:	LSFDGQKVYRTIANTDVAAWPNG----KIYFGVTKVDFSQYDDQKNETST			
CRY3BB:	LSFDGQKVYRTIANTDVAAWPNG----KVYLGVTKVDFSQYDDQKNETST			
CRY3BA:	LSFDGQKVYRTIANTDIAAFPDG----KIYFGVTKVDFSQYDDQKNETST			
CRY3A:	<u>LEFNGEKVYRAVANTNLAVWPSA----</u> <u>VYSGVTKVEFSQYNDQTDEAST</u>			
	+++	+++++	++++	+++++

FIG. 17B

	440	450	460	470	480
CRY3C:	QTYDSKRNVGGIV-FDSIDQLPPITTTDESLEKAYSHQLNRYVRCFLLQGG				
CRY3BB2:	QTYDSKRNNHVGGAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR				
CRY3BB:	QTYDSKRNNHVSQAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR				
CRY3BA:	QTYDSKRYNGYLGAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR				
CRY3A:	QTYDSKRNVGAVS-WDSIDQLPPETTDEPLEKGYSHQLNRYVMCFLMQGSR				
	++++	+++++			++++++

	490	500	510	520	530
CRY3C:	GIIPVFTWTHKSVDFYNTLDSEKITQIPFVKAFILVNSTSVVAGPGFTGG				
CRY3BB2:	GTIPFFTWTTHRSVDFNTIDAELITQLPVVKAYALSSGASIIIEGPGFTGG				
CRY3BB:	GTIPFFTWTTHRSVDFNTIDAELITQLPVVKAYALSSGASIIIEGPGFTGG				
CRY3BA:	GTIPFFTWTTHRSVDFNTIDAELITQLPVVKAYALSSGASIIIEGPGFTGG				
CRY3A:	GTIPVLTWTHKSVDFNMDSKKITQLPLVKAYKLQSGASVVAGPRFTGG				
	++++++	+++++	++++		++++++

	540	550	560	570	580
CRY3C:	DII-KCT-NGSGLTLYVTPAPDLTYSKTYKIRIRYASTSQVRFGIDLGSY				
CRY3BB2:	NLLFLKESSNSIAKFKVTL-NSAALLQRYRVIRIRYASTTNLRLRFVQNSNN				
CRY3BB:	NLLFLKESSNSIAKFKVTL-NSAALLQRYRVIRIRYASTTNLRLRFVQNSNN				
CRY3BA:	NLLFLKESSNSIAKFKVTL-NSAALLQRYRVIRIRYASTTNLRLRFVQNSNN				
CRY3A:	DII-QCTENGAATIIYVTPD--VSYSQKYRARIHYASTSQITFTLSLDGA				
	++++++	++++++	+++++	+++++	+++++

	590	600	610	620	630
CRY3C:	THSISYFDKTMKGNLTLYNSFNLSSVSRPIEISG-GNKIGVSVGGIGSG				
CRY3BB2:	DFIVIIYINKTMNIDDDLTYYQTFDLATTNSNMGFSGDTNELIIGAESFVSN				
CRY3BB:	DFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN				
CRY3BA:	DFLVIYINKTMNIDGDLTYQTFDFATSNMGSFGDTNDFIIGAESFVSN				
CRY3A:	PFNQYFDTINKGDLTLYNSFNLASFSTPFELSG--NNLQIGVTGLSAG				
	++++++	+++++	++++	+++++	+++++

	640	650
CRY3C:	DEVYIDKIEFIPMD	(SEQ ID NO:109)
CRY3BB2:	EKIYIDKIEFIPVQL	(SEQ ID NO:110)
CRY3BB:	EKIYIDKIEFIPVQL	(SEQ ID NO:111)
CRY3BA:	EKIYIDKIEFIPVQ	(SEQ ID NO:112)
CRY3A:	DKVYIDKIEFIPVN	(SEQ ID NO:113)
	+++++	

FIG. 17C